

Diagram from DR. BRUSCA at  
interview of 8-18-94

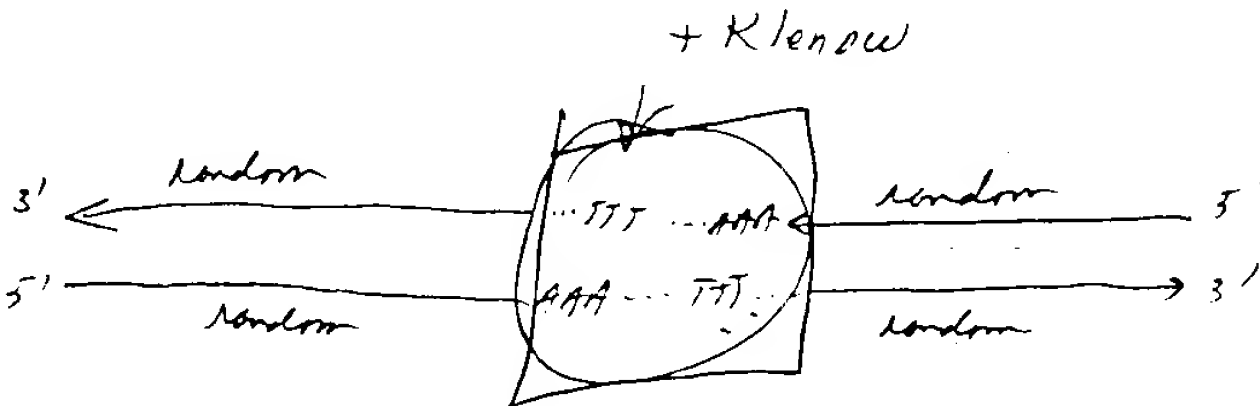
80100-01

1<sup>st</sup> method Kaufmann 5,723,323

1<sup>st</sup> strand  
(TdT) 5' → random → AAA...TTT... 3'

2<sup>nd</sup> strand 3' → TTT...AAA ← random 5'  
1<sup>st</sup> strand 5' → AAA...TTT... 3'

①



⇒ not totally  
random sequence.

②

Random has deficit of T to avoid stop codons.

2<sup>nd</sup> method

digest short (8mer) oligos without stop codons. (exemplified by 5 oligos  
each is a palindromic & forms ds DNA, digest them to form  
random oligomers of ds palindromes)

1 4 2 3 6 8 7 5

↓ ligase

=====

↓

insert to vector

⇒ not totally random sequence

also Chem 8 L 35-43 vague

For Pictures, Col. 14, say get them from the DNA clones.

or alternatively begins biochemical peptide synthesis scheme. Col. 15-16